

Gencore version 4.5
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OM protein - protein search, using sw model

Run on: March 1, 2001, 16:22:06 ; Search time 88.16 Seconds

(without alignments)
38.555 Million cell updates/sec

Title: US-09-331-631A-33
Perfect score: 77
Sequence: 1 CAXCXXXCXXXXXXXXXCAAXXXC 29

Scoring table: BLOSUM62DX
Gapop 10.0 , Gapext 0.5

Searched: 374700 seqs, 117207915 residues

Total number of hits satisfying chosen parameters: 374700

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPTREMBL_15:*

1: sp_archaea:*

2: sp_bacteria:*

3: sp_fungi:*

4: sp_human:*

5: sp_invertebrate:*

6: sp_mammal:*

7: sp_mhc:*

8: sp_organelle:*

9: sp_phage:*

10: sp_plant:*

11: sp_reptile:*

12: sp_virus:*

13: sp_vertebrate:*

14: sp_unclassified:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	77	100.0	43	5	Q9VDN2

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1	77	100.0	43	5	Q9VDN2

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Result No.	Score	Query Match	Length	DB ID	Description
1	77	100.0	43	5	Q9VDN2

ALIGNMENTS

RESULT	1
Q9VDN2	PRELIMINARY; PRT; 43 AA.
Q9VDN2; DT	01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT	01-JUN-2000 (TREMBLrel. 14, Last annotation update)
DE	CG5097 PROTEIN
GN	CG5097
OS	drosofilla melanogaster (fruit fly)
OC	Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydriidae; Drosophilidae; Drosophila.
OX	NCBI_TaxID=7227;
RN	[1]
RP	SEQUENCE FROM N.A.
RC	STRAIN-BERKELEY;
RX	Medline=20196005; Pubmed=10731132;
RA	Adams M.D., Celiker A.E., Holt R.A., Evans C.A., Gocayne J.D., Mauelides P.G., Scheiner S.E., Li P.W., Hoskins R.A., Galle R.F., George R.A., Lewis S.E., Richardson S.N., Sutton G.C., Lewin M.J., Richardson M.D., Zhang Q., Chen L.X., Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Preiffier B.D., Wan K.H., Boyle C., Baxter E.G., Heit G., Nelson C.R., Miklos G.I.G., Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D., Balliew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M., Beeson K.Y., Beto P.V., Berman B.P., Bhandari D., Bolshakov S., Borkova D., Botchan M.R., Bouck J., Brokstein P., Brotter P., Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I., Cherry J.M., Cawley S., Dahake C., Davenport L.B., Davies P., de Pablo B., Delcher A., Deng Z., May A.D., Dew I., Dietz S.M., Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Durbin R., Durbin K.J., Evangelista C.C., Ferrera S., Fleischmann W., Fosler C., Gabrilian A.E., Garg N.S., Gelbart W.M., Glasser K., Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M., Harris N.L., Harvey D., Hernandez J.R., Houck J., Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C., Jalali M., Kalish F., Karren G.H., Ke Z., Keim J.A., Ketchum K.A., Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z., Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X., Liu X., Mattei B., McIntosh M.P., McLeod M.P., McPherson D., Merkulov G., Milashina N.V., Mobarry C., Morris J., Moshefi A., Merkulov G., Milashina N.V., Mobarry C., Morris J., Moshefi A., O96388 perna virid

RA Mount S.M.; Moy M.; Murphy B.; Murphy L.; Muony D.M.; Nelson D.L.; RA Nelson D.R.; Nelson K.A.; Nixon K.; Nusslein-Volhard P.; Paclob J.M.; RA Palazzo M.; Pittman G.S.; Pan S.; Pollard J.; Puri V.; Reese M.G.; RA Reinert K.; Remington K.; Saunders R.D.C.; Scheeler F.; Shen H.; RA Shue B.C.; Siden-Kimmos I.; Simpson M.; Skupski M.P.; Smith T.; RA Spier E.; Spradling A.C.; Stapleton M.; Strong R.; Sun E.; RA Svirkas R.; Tector C.; Turner R.; Venter J.; Wang A.H.; Wang X.; RA Wang Z.-Y.; Wasserman D.A.; Weinstock G.M.; Weissbach J.; RA Williams S.M.; Woodage T.; Worley K.C.; Wu D.; Yao Q.A.; RA Ye J.; Yeh R.-F.; Zaveri J.S.; Zhan M.; Zhang G.; Zhao Q.; Zheng L.; RA Zheng X.H.; Zhong N.; Zhong W.; Zhou X.; Zhu S.; Zhu X.; Smith H.O.; RA Gibbs R.A.; Myers E.W.; Rubin G.M.; Venter J.C.; RA RT "The genome sequence of *Drosophila melanogaster*."; RA RIL Science 287: 2185-2195 (2000). RA RIL EMBL; AE003730; AAFF57581; -. RA RIL FLYBASE; FBgn0038790; CG5097. RA RIL INTERPRO; IPR000561; -. RA RIL INTERPRO; IPR000966; -. RA RIL PFAM; PF0067; Metallothionein; 1. RA RIL PRINTS; PS00872; MTDIPTERA. RA RIL PROSITE; PS00022; EGF_1; UNKNOWN_1. RA RIL SEQUENCE; 43 AA; 4597 MW; B54E72B14B89DFE CRC64;

Query Match 100.0%; Score 77; DB 5; Length 43; RA Matches 6; Conservative 23; Mismatches 0; Indels 0; Gaps 0; RA

OY 1 CXXCXXXCXXXXXXXXXXXXXXCXXC 29 RA

Db 3 CKGGTNCCKCDTKCGDNCAcnODCKVC 31 RA

RESULT 2 RA

ID 023947 RA

AC 023947; PRELIMINARY; PRT; 49 AA. RA

DT 01-NOV-1996 (TREMBLrel. 01, Created) RA

DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update) RA

DT 01-OCT-2000 (TREMBLrel. 15, Last annotation update) RA

DE TESTIS-SPECIFIC RNA. RA

GN DHTC3. RA

OS Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; RA

OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; RA

OC Ephydriidae; Drosophilidae; Drosophila; RA

OX NCBI_TaxID:7224; RA

DR EMBL; X58114; CA41118.1; -. RA

DR FLYBASE; FBgn0035097; Dhyd\Mst87Fb. RA

DR INTERPRO; IPR001450; -. RA

DR PROSITE; PS00198; 4Fe4S_FERRREDOXIN; UNKNOWN_1. RA

DR SEQUENCE 49 AA; 4550 MW; 24758FEC51369F01 CRC64;

Query Match 100.0%; Score 77; DB 5; Length 49; RA

Matches 6; Conservative 23; Mismatches 0; Indels 0; Gaps 0; RA

OY 1 CXXCXXXCXXXXXXXXXXXXXXCXXC 29 RA

Db 3 CGPCGGCCGGGGCPYSCCGPcYSCC 31 RA

RESULT 4 RA

ID 09XVX3 RA

AC 09XVX3; PRELIMINARY; PRT; 152 AA. RA

DT 01-NOV-1999 (TREMBLrel. 12, Created) RA

DT 01-NOV-1999 (TREMBLrel. 12, Last sequence update) RA

DT 01-MAY-2000 (TREMBLrel. 13, Last annotation update) RA

DE C06A16 PROTEIN. RA

GN C06A16. RA

OS Caenorhabditis elegans. RA

OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea; RA

OC Rhabditidae; Peioderinae; Caenorhabditis. RA

OX NCBI_TaxID:6239; RA

RN [1] RA

RP SEQUENCE FROM N.A. RA

RA MEDLINE=94150718; PubMed=7906398; RA

RA Monmurray A.; RA

RT "2.2 Mb of contiguous nucleotide sequence from chromosome III of *C. elegans*."; RA

RT Submitted (JUN-1995) to the EMBL/GenBank/DBJ databases. RA

RL SEQUENCE FROM N.A. RA

RL [12] RA

RA SEQUENCE FROM N.A. RA

RA -MEDLINE=94150718; PubMed=7906398; RA

RA Wilson R.; Ainscough R.; Anderson K.; Baynes C.; Berks M.; RA Bonfield J.; Burton J.; Connell M.; Corsey T.; Cooper J.; Coulson A.; RA Craxton M.; Dear S.; Du Z.; Durbin R.; Favello A.; Fulton L.; RA Gardner A.; Green P.; Hawkins T.; Hillier L.; Jier M.; Johnston L.; RA Jones M.; Kershaw J.; Kirstein J.; Laister N.; Latrellie P.; RA Lightning J.; Lloyd C.; Monmurray A.; Mortimore B.; O'Callaghan M.; RA Parsons J.; Percy C.; Riker L.; Roopra A.; Saunders D.; Showken R.; RA Smalton N.; Smith A.; Sonnhammer E.; Straden R.; Sulston J.; RA Thierry-Mieg J.; Thomas K.; Vaudin M.; Vaughan K.; Waterston R.; RA Watson A.; Weinstock L.; Wilkinson-Sproat J.; Wohldman P.; RA RT "2.2 Mb of contiguous nucleotide sequence from chromosome III of *C. elegans*."; RA

RA Nature 368:32-37 (1994). RA

RA EMBL; Z49886; CA90055.1; -. RA

DR INTERPRO; IPR000561; -. RA

DR INTERPRO; IPR001450; -. RA

DR INTERPRO; IPR001502; -. RA

DR PROSITE; PS00022; EGF_1; UNKNOWN_1. RA

DR PROSITE; PS00198; 4Fe4S_FERRREDOXIN; UNKNOWN_1. RA

DR PROSITE; PS00764; ENDONUCLEASE_III_1; 1. RA

DR PROSITE; PS01208; VNFC; UNKNOWN_1. RA

RA Jones M., Kershaw J., Kirsten J., Laister N., Latreille P.,
 RA Lightning J., Lloyd C., McMurray A., Mortimore B., O'Callaghan M.,
 RA Parsons J., Percy C., Riffen L., Roopra A., Saunders D., Shownkeen R.,
 RA Smalton N., Smith A., Sonhammer E., Staden R., Sulston J.,
 RA Thirrey-Mieg J., Thomas K., Vaudin M., Vaughan K., Waterston R.,
 RA Watson A., Weinstock L., Wilkinson-Sproat J., Wohldman P.;
 RT elegans. ";
 RL "2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BRISTOL N2;
 RA Leimbach D.;
 RL Submitted (JAN-1996) to the EMBL/GenBank/DDJB databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BRISTOL N2;
 RA Waterston R.;
 RL Submitted (APR-1997) to the EMBL/GenBank/DDJB databases.
 DR EMBL: U46575; AAB5245.1; -;
 SQ SEQUENCE 273 AA; 29231 MW; 11542812CC566530 CRC64;
 RESULT 8
 Q23390 PRELIMINARY; PRT; 314 AA.
 AC Q23390
 DT 01-NOV-1996 (TREMBLrel. 01, Created)
 DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
 DE ZK1057.7. PROTEIN.
 GN K1057.7.
 OS Caenorhabditis elegans.
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidae;
 OC Rhabditidae; Pelerodidae; Caenorhabditis;
 OC NCBI-TaxID=6239;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Thomas K.;
 RL Submitted (MAR-1996) to the EMBL/GenBank/DDJB databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 MEDLINE=4150718; PubMed=7905398;
 RA Wilson R., Ainscough R., Anderson K., Baynes C., Berks M., Berks M.,
 RA Bonfield J., Burton J., Connell M., Copey T., Cooper J., Coulson A.,
 RA Craxton M., Dear S., Du Z., Durbin R., Favello A., Fulton L.,
 RA Gardner A., Green P., Hawkins T., Hillier L., Jier M., Johnston L.,
 RA Jones M., Kershaw J., Kirsten J., Laister N., Latreille P.,
 RA Lightning J., Lloyd C., McMurray A., Mortimore B., O'Callaghan M.,
 RA Parsons J., Percy C., Riffen L., Roopra A., Saunders D., Shownkeen R.,
 RA Smalton N., Smith A., Sonhammer E., Staden R., Sulston J.,
 RA Thirrey-Mieg J., Thomas K., Vaudin M., Vaughan K., Waterston R.,
 RA Watson A., Weinstock L., Wilkinson-Sproat J., Wohldman P.;
 RT elegans. ";
 RL "2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
 DR EMBL: Z70038; CAAG9386.1; -;
 SQ SEQUENCE 314 AA; 32803 MW; 8735F50B826ED303 CRC64;

Query Match 100.0%; Score 77; DB 5; Length 314;
 Best Local Similarity 20.7%; Pred. No. 22;
 Matches 6; Conservative 23; Mismatches 0; Indels 0; Gaps 0;

QY 1 CXXCXXCXXXXXXCXXCXXC 29

DB 214 C5TCNNCPSCISQANCIPOCMRPLPTC 242

RESULT 9
 Q083828 PRELIMINARY; PRT; 325 AA.
 ID 083828
 AC 083828;
 DT 01-NOV-1998 (TREMBLrel. 08, Created)
 DT 01-MAY-2000 (TREMBLrel. 13, Last annotation update)
 DE HYPOTHETICAL 34.1 KDA PROTEIN.
 GN TP0856.
 OC Treponema pallidum.
 OX Bacteria; Spirochaetales; Spirochaetaceae; Treponema.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=NICHOOLS;
 RX MEDLINE=98332270; PubMed=9665876;
 RA Fraser C.M., Norris S.J., Weinstock G.M., White O., Sutton G.G.,
 RA Dodson R., Gwinn M., Hickey E.K., Clayton R., Ketchum K.A.,
 RA Sodergren E., Hardham J.M., McLeod M.P., Salzberg S., Peterson J.,
 RA Khalak H., Richardson D., Howell J.K., Chidambaram M., Utterback T.,
 RA McDonald L., Artiach P., Bowman C., Cottam M.D., Fujii C., Garland S.,
 RA Hatch B., Horst K., Roberts K., Sandusky M., Weidman J., Smith H.O.,
 RA Venter J.C.,
 RT "Complete genome sequence of Treponema pallidum, the syphilis
 RT spirochete.;"
 RL Science 281:375-388(1998);
 DR EMBL: AE001256; AAC05828.1;
 TIGR; TP0056; -.
 KW Hypothetical protein.
 SQ SEQUENCE 325 AA; 34054 MW; F9CFDCBD253C07D2 CRC64;

Query Match 100.0%; Score 77; DB 2; Length 325;
 Best Local Similarity 20.7%; Pred. No. 22;
 Matches 6; Conservative 23; Mismatches 0; Indels 0; Gaps 0;

QY 1 CXXCXXCXXXXXXCXXCXXC 29

DB 238 C5TCNNCPSCISQANCIPOCMRPLPTC 266

RESULT 10
 Q09SPL3 PRELIMINARY; PRT; 625 AA.
 ID 09SPL3
 AC 09SPL3;
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
 DT 01-OCT-2000 (TREMBLrel. 15, Last annotation update)
 DE VICKIIN PRECURSOR (FRAGMENT).
 GN AMP2.
 OS Macadamia integrifolia (Macadamia nut).
 OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
 OC Magnoliophyta; eudicotyledons; Proteaceae; Macadamia.
 OX NCBI-TaxID=60698;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE-NUT KERNEL;
 RA Marcus J.P., Goultier K.C., Green J.L., Manners J.M.,
 RT "A family of antimicrobial peptides is produced by processing of a 7S
 RT globulin protein in Macadamia integrifolia.";
 RL Plant J. 0:0(1999);
 DR EMBL: AF61185; AAC54245.1; -.
 HSSP; P02853; 2PFL.

DR INTERPRO; IPR001113; -.
 DR PFAM; PF00546; Seedstore_7s; 1.
 FT NON_TER 1
 SEQUENCE 625 AA; 73586 MN; 415808A89B370296 CRC64;
 SQ

Query Match 100.0%; Score 77; DB 10; Length 625;
 Best local similarity 20.7%; Pred. No. 33;
 Matches 6; Conservative 23; Mismatches 0;
 Indels 0; Gaps 0;

Qy 1 CXXCXXXXXXCXXXXXXCXXXXCXXC 29
 Db 41 COOCORRCROOESDPROQQYCORRCBIC 69

RESULT 11
 09SPL5 PRELIMINARY; PRT; 666 AA.
 ID 09SPL5
 AC 09SPL5;
 DT 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
 DT 01-OCT-2000 (TREMBLrel. 15, Last annotation update)
 DE VICTILIN PRECURSOR.
 GN AMP2.
 OS Macadamia integrifolia (Macadamia nut).
 OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
 OC Magnoliophyta; eudicotyledons; Proteaceae; Macadamia.
 OX NCBI_TaxId=60698;
 RN [1]
 RP
 RC TISSUE-NUT KERNEL;
 RA Marcus J.P., Goultier K.C., Green J.L., Manners J.M.;
 RT 'A family of antimicrobial peptides is produced by processing of a 7 S
 RL globulin protein in Macadamia integrifolia kernels.';
 DR EMBL; AF161883; RAD5/244.1; -.
 DR HSSP; P02853; 2PML;
 DR INTERPRO; IPR001113; -.
 DR PFAM; PF00546; Seedstore_7s; 1.
 DR SEQUENCE 666 AA; 78217 MN; C752B884B2DF0224 CRC64;
 SQ

Query Match 100.0%; Score 77; DB 10; Length 666;
 Best local similarity 20.7%; Pred. No. 34;
 Matches 6; Conservative 23; Mismatches 0;
 Indels 0; Gaps 0;

Qy 1 CXXCXXXXXXCXXXXXXCXXXXCXXC 29
 Db 82 COQCQRRCROOESDPROQQYCORRCBIC 110

RESULT 12
 09SPL4 PRELIMINARY; PRT; 666 AA.
 ID 09SPL4
 AC 09SPL4;
 DT 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
 DT 01-OCT-2000 (TREMBLrel. 15, Last annotation update)
 DE VICTILIN PRECURSOR.
 GN AMP2.
 OS Macadamia integrifolia (Macadamia nut).
 OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
 OC Magnoliophyta; eudicotyledons; Proteaceae; Macadamia.
 OX NCBI_TaxId=60698;
 RN [1]
 RP
 RC TISSUE-NUT KERNEL;
 RA Marcus J.P., Goultier K.C., Green J.L., Manners J.M.;
 RT 'A family of antimicrobial peptides is produced by processing of a 7 S
 RL globulin protein in Macadamia integrifolia.';
 DR EMBL; AF161884; RAD5/245.1; -.
 DR HSSP; P02853; 2PML.

RESULT 13
 09PVG7 PRELIMINARY; PRT; 39 AA.
 ID 09PVG7
 AC 09PVG7;
 DT 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
 DT 01-MAY-2000 (TREMBLrel. 13, Last annotation update)
 DE RECEPTOR TYROSINE KINASE XMRK (FRAGMENT).
 GN XMRK.
 OS Xiphophorus maculatus (Southern platyfish).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Buteleosteii; Neoteleosteii;
 OC Acanthopterygii; Percomorpha; Atherinomorpha;
 OC Cyprinodontiformes; Poeciliidae; Xiphophorus.
 OX NCBI_TaxID=8083;
 RN [1]
 RP
 RC STRAIN-SR;
 RA MEDLINE-99126443; PubMed=9927468;
 RT Gutbrod H., Schartl M.;
 RT 'Intragenic sex-chromosomal crossovers of Xmrk oncogene alleles affect
 pigment pattern formation and the severity of melanoma in
 Xiphophorus'; Neopterygii; Teleostei; Buteleosteii; Neoteleosteii;
 RT Genetics 151:773-783(1999);
 RL EMBL; AF092693; RAD03714.1; -.
 KW Receptor; Kinase.
 FT NON_TER 1
 FT NON_TER 39
 SQ SEQUENCE 39 AA; 4195 MN; 42303BA05F6DB557 CRC64;

Query Match 88.3%; Score 68; DB 13; Length 39;
 Best local similarity 17.9%; Pred. No. 36;
 Matches 5; Conservative 23; Mismatches 0;
 Indels 0; Gaps 0;

Qy 2 XXCXXXXXXCXXXXXXCXXXXCXXC 29
 Db 3 LLCAE0CNRGRGPKIDCCNEHCAGGC 30

RESULT 14
 016861 PRELIMINARY; PRT; 46 AA.
 ID 016861
 AC 016861;
 DT 01-NOV-1996 (TREMBLrel. 01, Created)
 DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
 DT 01-AUG-1998 (TREMBLrel. 07, Last annotation update)
 DE CYSTEINE-RICH PROTEIN (FRAGMENT).
 OS Homo sapiens (Human).
 OC Mammalia; Eutheria; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Cetartiodactyla; Hominoidea; Homo.
 OX NCBI_TaxId=9606;
 RN [1]
 RP
 RA SEQUENCE FROM N_A.
 RA Lemasson I., Devaux C., Messard J.M.;
 RL Submitted (JUL-1996) to the EMBL/GenBank/DDBJ databases.
 DR EMBL; U63332; AAB05810.1; -.
 FT NON_TER 1
 SQ SEQUENCE 46 AA; 5061 MN; 311922FE40A44E8F CRC64;

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Search completed: March 1, 2001, 16:22:07
Job time: 284 sec

Qy          2  XCXXXXCXXXXXXXCXXXXCXXXC  29
Db          2  SECQORCSYRCSATSHKKPCKMFQKCC 29

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Search completed: March 1, 2001, 16:22:07
Job time: 284 sec

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